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Xu, Wenfeng
Madden, Karen
Yee, David P.

<130> 98-75

<151> 1999-01-07

<151> 1999-12-09

<170> FastSEQ for Windows Version 3.0

<211> 1192

<213> Homo sapiens

<221> CDS

 $\langle 400 \rangle$ 1

gac cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag 98
Asp Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys
20 25 30

ttc	tat	gac	cat	ctc	ctg	agg	gac	tgc	atc	agc	tgt	gcc	tcc	atc	tgt	146
Phe	Tyr	Asp	His	Leu	Leu	Arg	Asp	Cys	Ile	Ser	Cys	Ala	Ser	Ile	Cys	
			35					40					45			

act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag 674
Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln
210 215 220

cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct 722
 Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro
 225 230 235

gcc cag gag ggg ggc cca ggt gca taaatggggg tcaggaggagg aaaggaggag 776
 Ala Gln Glu Gly Gly Pro Gly Ala
 240 245

ggagagagat ggagaggagg ggagagagaa agagaggttg ggagagggga gagagatatg 836
 aggagagaga gacagaggag gcagagaggg agagaaacag aggagacaga gaggagagaga 896
 gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga ggcagagaag 956
 gaaagaggca gagagggaga gaggcagaga gggagagagg cagagagaca gagagggaga 1016
 gagggacaga gagagataga gcaggaggtc ggggcactct gagtcccagt tcccagtgca 1076
 gctgtagggtc gtcatcacct aaccacacgt gcaataaagt cctcgtgcct gctgctcaca 1136
 gcccccgaga gccctcctc ctggagaata aaacctttgg cagctgccct tcctca 1192

<210> 2

<211> 247

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
 20 25 30
 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
 35 40 45
 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
 50 55 60
 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
 65 70 75 80
 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
 85 90 95
 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
 100 105 110
 Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val
 115 120 125
 Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly
 130 135 140
 Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala
 145 150 155 160
 Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr
 165 170 175
 Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg

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<210> 3
<211> 360
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(360)
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<400> 3

cag gag gag cgc tgg tca ctc agc tgc cgc aag gag caa ggc aag ttc 96
Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
20 25 30

tat	gac	cat	ctc	ctg	agg	gac	tgc	atc	agc	tgt	gcc	tcc	atc	tgt	gga	144
Tyr	Asp	His	Leu	Leu	Arg	Asp	Cys	Ile	Ser	Cys	Ala	Ser	Ile	Cys	Gly	
		35					40					45				

cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc 192
Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
50 55 60

cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt 240
Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
65 70 75 80

gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga 288
Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
85 90 95

ggc tca gaa gca agt cca gct ctc ccg ggg ctg aaq ctg agt qca qat 336

Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
 100 105 110

cag gtg gcc ctg gtc tac agc acg
 Gln Val Ala Leu Val Tyr Ser Thr
 115 120

360

<210> 4
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Trp Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe
 20 25 30
 Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly
 35 40 45
 Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser
 50 55 60
 Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val
 65 70 75 80
 Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg
 85 90 95
 Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp
 100 105 110
 Gln Val Ala Leu Val Tyr Ser Thr
 115 120

<210> 5
 <211> 1377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (14)...(895)

<400> 5

agcatcctga gta atg agt ggc ctg ggc cgg agc agg cga ggt ggc cgg
 Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg
 1 5 10

49

agc cgt gtg gac cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg	97
Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly	
15 20 25	
gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg	145
Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu	
30 35 40	
ggt acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc	193
Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg	
45 50 55 60	
acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc	241
Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly	
65 70 75	
aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc	289
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile	
80 85 90	
tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc	337
Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu	
95 100 105	
agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga	385
Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly	
110 115 120	
gaa gtt gaa aac aat tca gac aac tcg gga agg tac caa gga ttg gag	433
Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu	
125 130 135 140	
cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt	481
His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser	
145 150 155	
gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt	529
Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys	
160 165 170	
gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag	577
Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys	
175 180 185	
agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt	625

004070-95954460

Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser	
190 195 200	
ccg gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg	673
Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val	
205 210 215 220	
agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag	721
Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu	
225 230 235	
tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac	769
Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp	
240 245 250	
ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg	817
Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu	
255 260 265	
cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg	865
Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val	
270 275 280	
cct gcc cag gag ggg ggc cca ggt gca taa atgggggtca gggagggaaa	915
Pro Ala Gln Glu Gly Gly Pro Gly Ala *	
285 290	
ggaggagggga gagagatgga gaggagggga gagagaaaga gaggtgggga gaggggagag	975
agatatgagg agagagagac agaggaggca gaaagggaga gaaacagagg agacagagag	1035
ggagagagag acagagggag agagagacag aggggaagag aggcagagag ggaaagaggc	1095
agagaaggaa agagacaggc agagaaggag agaggcagag agggagagag gcagagaggg	1155
agagaggcag agagacagag agggagagag ggacagagag agatagagca ggaggtcggg	1215
gcactctgag tcccagttcc cagtgcagct gtaggtcgtc atcacctaac cacacgtgca	1275
ataaagtcct cgtgcctgct gctcacagcc cccgagagcc cctcctcctg gagaataaaa	1335
cctttggcag ctgcccttcc tcaaaaaaaaa aaaaaaaaaa aa	1377

<210> 6
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
1 5 10 15
Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg

20 25 30
 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
 35 40 45
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50 55 60
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65 70 75 80
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85 90 95
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
 165 170 175
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
 180 185 190
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
 195 200 205
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
 210 215 220
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
 225 230 235 240
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
 245 250 255
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
 260 265 270
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
 275 280 285
 Gly Gly Pro Gly Ala
 290

<210> 7
 <211> 995
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (219)...(773)


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aagactcaaa cttagaaact tgaattagat gtggtattcaaatccttacg tgccgcgaag      60
acacagacag cccccgtaag aaccacgaa gcaggcgaaagtcatgttc tcaacattct    120
agctgctctt gctgcatttg ctctggaatt cttgtagaga tattacttgt ccttccaggc    180
tgttctttct gtagctccct tgttttcttt ttgtgatc atg ttg cag atg gct ggg    236
                               Met Leu Gln Met Ala Gly
                               1             5
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gaa ggc gca acc att ctt gtc acc acg aaa acg aat gac tat tgc aag 716

<400> 8															
Met 1	Leu	Gln	Met	Ala 5	Gly	Gln	Cys	Ser	Gln 10	Asn	Glu	Tyr	Phe	Asp 15	Ser
Leu	Leu	His	Ala 20	Cys	Ile	Pro	Cys	Gln 25	Leu	Arg	Cys	Ser	Ser 30	Asn	Thr
Pro	Pro	Leu	Thr	Cys	Gln	Arg	Tyr 40	Cys	Asn	Ala	Ser	Val 45	Thr	Asn	Ser
Val	Lys 50	Gly	Thr	Asn	Ala	Ile 55	Leu	Trp	Thr	Cys	Leu 60	Gly	Leu	Ser	Leu
Ile 65	Ile	Ser	Leu	Ala 70	Val	Phe	Val	Leu	Met 75	Phe	Leu 80	Leu	Arg	Lys	Ile
Ser	Ser	Glu	Pro	Leu 85	Lys	Asp	Glu	Phe 90	Lys	Asn	Thr 95	Gly	Ser	Gly	Leu
Leu	Gly	Met	Ala 100	Asn	Ile	Asp	Leu 105	Glu	Lys	Ser	Arg 110	Thr	Gly	Asp	Glu
Ile	Ile	Leu	Pro	Arg	Gly	Leu 115	Glu 120	Tyr	Thr	Val	Glu 125	Glu	Cys	Thr	Cys
Glu 130	Asp	Cys	Ile	Lys	Ser	Lys 135	Pro	Lys	Val	Asp 140	Ser	Asp	His	Cys	Phe
Pro 145	Leu	Pro	Ala	Met	Glu 150	Glu	Gly	Ala	Thr	Ile 155	Leu	Val	Thr	Thr	Lys
Thr	Asn	Asp	Tyr	Cys 165	Lys	Ser	Leu	Pro	Ala 170	Ala	Leu	Ser	Ala	Thr 175	Glu
Ile	Glu	Lys	Ser	Ile	Ser	Ala	Arg								

<220>

<223> Motif describing the cysteine-rich pseudo-repeat domain

<221> VARIANT

<222> (1)...(2)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<221> VARIANT

<222> (4)...(4)

<223> Xaa is any amino acid residue except cysteine.

<221> VARIANT

<222> (5)...(5)

<223> Xaa is glutamine, glutamic acid, or lysine.

<221> VARIANT

<222> (6)...(6)

<223> Xaa is glutamine, glutamic acid, lysine, asparagine, arginine, aspartic acid, histidine, or serine.

<221> VARIANT

<222> (7)...(7)

<223> Xaa is glutamine or glutamic acid.

<221> VARIANT

<222> (8)...(9)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<221> VARIANT

<222> (10)...(11)

<223> Xaa is tyrosine, phenylalanine, or tryptophan.

<221> VARIANT

<222> (13)...(13)

<223> Xaa is any amino acid residue except cysteine.

<221> VARIANT

<222> (16)...(17)

<223> Each Xaa is independently any amino acid residue

except cysteine.

<221> VARIANT

 $\langle 222 \rangle \quad (19) \dots (19)$

<223> Xaa is isoleucine, methionine, leucine, or valine.

<221> VARIANT

 $\langle 222 \rangle \quad (20) \dots (20)$

<223> Xaa is any amino acid residue except cysteine.

<221> VARIANT

<222> (22) ... (24)

<223> Each Xaa is independently any amino acid residue except cysteine.

<221> VARIANT

 $\langle 222 \rangle \quad (26) \dots (31)$

<223> Each Xaa is independently any amino acid residue except cysteine.

<221> VARIANT

<222> (32) ... (33)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<221> VARIANT

<222> (35)...(36)

<223> Each Xaa is independently any amino acid residue except cysteine.

<221> VARIANT

 $\langle 222 \rangle \quad (37) \dots (37)$

<223> Xaa is tyrosine or phenylalanine.

<221> VARIANT

<222> (39) . . . (40)

<223> Each Xaa is independently any amino acid residue except cysteine, or absent.

<400> 10

Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa Leu Leu Xaa
1 5 10 15
Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa

35

40

<210> 11

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide sequence encoding the polypeptide of SEQ ID NO:4

<221> variation

<222> (1)...(360)

<223> Each N is independently A, T, G, or C.

<400> 11

atgwsnggny	tnggnmgnws	nmgnmgnggn	ggnmgnwsnm	gngtngayca	rgargarmgn	60
tggwsnytnw	sntgymgnaa	rgarcarggn	aarttytayg	aycayytnyt	nmngnaytgy	120
athwsntgyg	cnwsnathtg	yggncarcay	ccnaarcart	gygcntaytt	ytgygaraay	180
aarytnmgnw	sncngtnaa	yytnccnccn	garytnmgnm	gncarmgnws	ngngngargtn	240
garaayaayw	sngayaayws	nggnmgntay	carggnytn	arcaymgngg	nwsngargcn	300
wsnccngcny	tnccnggnyt	naarytnwsn	gcngaycarg	tngcnytngt	ntaywsnacb	360

<210> 12

<211> 741

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide sequence encoding a polypeptide of SEQ ID NO:2

<221> variation

<222> (1)...(741)

<223> Each N is independently A, T, G, or C.

<400> 12

atgwsnggny	tnggnmgnws	nmgnmgnggn	ggnmgnwsnm	gngtngayca	rgargarmgn	60
tggwsnytnw	sntgymgnaa	rgarcarggn	aarttytayg	aycayytnyt	nmngnaytgy	120
athwsntgyg	cnwsnathtg	yggncarcay	ccnaarcart	gygcntaytt	ytgygaraay	180
aarytnmgnw	sncngtnaa	yytnccnccn	garytnmgnm	gncarmgnws	ngngngargtn	240
garaayaayw	sngayaayws	nggnmgntay	carggnytn	arcaymgngg	nwsngargcn	300
wsnccngcny	tnccnggnyt	naarytnwsn	gcngaycarg	tngcnytngt	ntaywsnacb	360
ytnggnytn	gytntgygc	ngtnytn	tygttytn	tngcngtngc	ntgyttytn	420
aaraarmgng	gngayccntg	ywsntgyca	ccnmgnwsnm	gnccnmgnca	rwsnccngcn	480

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aarwsnwsnc argaycaygc natggargcn ggnwsnccng tnwsnacnws nccngarccn 540
gtngaracnt gywsnttytg yttyccngar tgygmngcnc cnacncarga rwsngcngtn 600
acnccnggna cncngaycc nactgygcg ggnmgntggg gntgycayac nmgnacnacn 660
gtnytncarc cntgyccnca yathccngay wsnggnytn gnathtntg ygtncnccngcn 720
cargarggng gncnccngngc n 741

```

```

<210> 13
<211> 8
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> FLAG tag

```

```

<400> 13
Asp Tyr Lys Asp Asp Asp Asp Lys
1          5

```

```

<210> 14
<211> 7
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Glu-Glu tag

```

```

<400> 14
Glu Glu Tyr Met Pro Met Glu
1          5

```

```

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> Oligonucleotide ZC19980

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```

<400> 15
cgaagagcag tactgggatc ctct 24

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<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

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<223> Oligonucleotide ZC19981

gccaaggcca ctgtctggga tgt

23

<213> Homo sapiens

<222> (236)...(1027)

gaattcggca	cgaggcagaa	aggagaaaat	tcaggataac	tctcctgagg	ggtgagccaa	60
gccctgccat	gtagtgcacg	caggacatca	acaaacacag	ataacaggaa	atgatccatt	120
ccctgtggtc	acttattcta	aaggcccaa	ccttcaaagt	tcaagtagtg	atatggatga	180
ctccacagaa	agggagcagt	cacgccttac	ttcttgcctt	aagaaaagag	aagaa atg	238
					Met	
					1	

aaa ctg aag gag tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct 286
Lys Leu Lys Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser
5 10 15

gtc cga tcc tcc aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg 334
Val Arg Ser Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu
20 25 30

gca ctg ctg tct tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc 382
Ala Leu Leu Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala
35 40 45

gcc ctg caa ggg gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac 430
Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His
50 55 60 65

cac gcg gag aag ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg 478
His Ala Glu Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu
70 75 80

gag gaa gct cca gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca 526

Glu	Glu	Ala	Pro	Ala	Val	Thr	Ala	Gly	Leu	Lys	Ile	Phe	Glu	Pro	Pro	
			85					90					95			
gct	cca	gga	gaa	ggc	aac	tcc	agt	cag	aac	agc	aga	aat	aag	cgt	gcc	574
Ala	Pro	Gly	Glu	Gly	Asn	Ser	Ser	Gln	Asn	Ser	Arg	Asn	Lys	Arg	Ala	
		100					105					110				
gtt	cag	ggt	cca	gaa	gaa	aca	gtc	act	caa	gac	tgc	ttg	caa	ctg	att	622
Val	Gln	Gly	Pro	Glu	Glu	Thr	Val	Thr	Gln	Asp	Cys	Leu	Gln	Leu	Ile	
	115					120					125					
gca	gac	agt	gaa	aca	cca	act	ata	caa	aaa	gga	tct	tac	aca	ttt	gtt	670
Ala	Asp	Ser	Glu	Thr	Pro	Thr	Ile	Gln	Lys	Gly	Ser	Tyr	Thr	Phe	Val	
130					135					140					145	
cca	tgg	ctt	ctc	agc	ttt	aaa	agg	gga	agt	gcc	cta	gaa	gaa	aaa	gag	718
Pro	Trp	Leu	Leu	Ser	Phe	Lys	Arg	Gly	Ser	Ala	Leu	Glu	Glu	Lys	Glu	
				150					155					160		
aat	aaa	ata	ttg	gtc	aaa	gaa	act	ggc	tac	ttt	ttt	ata	tat	ggt	cag	766
Asn	Lys	Ile	Leu	Val	Lys	Glu	Thr	Gly	Tyr	Phe	Phe	Ile	Tyr	Gly	Gln	
			165					170					175			
gtt	tta	tat	act	gat	aag	acc	tac	gcc	atg	gga	cat	cta	att	cag	agg	814
Val	Leu	Tyr	Thr	Asp	Lys	Thr	Tyr	Ala	Met	Gly	His	Leu	Ile	Gln	Arg	
		180					185					190				
aag	aag	gtc	cat	gtc	ttt	ggg	gat	gaa	ttg	agt	ctg	gtg	act	ttg	ttt	862
Lys	Lys	Val	His	Val	Phe	Gly	Asp	Glu	Leu	Ser	Leu	Val	Thr	Leu	Phe	
	195					200					205					
cga	tgt	att	caa	aat	atg	cct	gaa	aca	cta	ccc	aat	aat	tcc	tgc	tat	910
Arg	Cys	Ile	Gln	Asn	Met	Pro	Glu	Thr	Leu	Pro	Asn	Asn	Ser	Cys	Tyr	
210					215					220					225	
tca	gct	ggc	att	gca	aaa	ctg	gaa	gaa	gga	gat	gaa	ctc	caa	ctt	gca	958
Ser	Ala	Gly	Ile	Ala	Lys	Leu	Glu	Glu	Gly	Asp	Glu	Leu	Gln	Leu	Ala	
				230					235					240		
ata	cca	aga	gaa	aat	gca	caa	ata	tca	ctg	gat	gga	gat	gtc	aca	ttt	1006
Ile	Pro	Arg	Glu	Asn	Ala	Gln	Ile	Ser	Leu	Asp	Gly	Asp	Val	Thr	Phe	
			245					250					255			
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Phe	Gly	Ala	Leu	Lys	Leu	Leu										

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260

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<211> 264

<212> PRT

<213> Homo sapiens

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 Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val
 35 40 45
 Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly
 50 55 60
 His His Ala Glu Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly
 65 70 75 80
 Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro
 85 90 95
 Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg
 100 105 110
 Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu
 115 120 125
 Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe
 130 135 140
 Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys
 145 150 155 160
 Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly
 165 170 175
 Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln
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 Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu
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 Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys
 210 215 220
 Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu
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Met Ala Met Ala Phe	
1 5	
tgc ccc aaa gat cag tac tgg gac tcc tca agg aaa tcc tgt gtc tcc	164
Cys Pro Lys Asp Gln Tyr Trp Asp Ser Ser Arg Lys Ser Cys Val Ser	
10 15 20	
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Cys Ala Leu Thr Cys Ser Gln Arg Ser Gln Arg Thr Cys Thr Asp Phe	
25 30 35	
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Cys Lys Phe Ile Asn Cys Arg Lys Glu Gln Gly Arg Tyr Tyr Asp His	
40 45 50	
ctc ctg ggg gcc tgc gtc agc tgt gac tcc acc tgc aca cag cac cct	308
Leu Leu Gly Ala Cys Val Ser Cys Asp Ser Thr Cys Thr Gln His Pro	
55 60 65	
cag cag tgt gcc cac ttc tgt gag aaa agg ccc aga agc cag gcg aac	356
Gln Gln Cys Ala His Phe Cys Glu Lys Arg Pro Arg Ser Gln Ala Asn	
70 75 80 85	
ctc cag ccc gag ctc ggg aga cca cag gcc ggg gag gtg gaa gtc agg	404
Leu Gln Pro Glu Leu Gly Arg Pro Gln Ala Gly Glu Val Glu Val Arg	
90 95 100	
tca gac aac tca gga agg cac cag gga tct gag cat ggt cca gga ttg	452
Ser Asp Asn Ser Gly Arg His Gln Gly Ser Glu His Gly Pro Gly Leu	
105 110 115	
agg cta agt agc gac cag ctg act ctc tac tgc aca ctg ggg gtc tgc	500

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Arg	Leu	Ser	Ser	Asp	Gln	Leu	Thr	Leu	Tyr	Cys	Thr	Leu	Gly	Val	Cys	
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ctc	tgc	gcc	atc	ttc	tgc	tgt	ttc	ttg	gtg	gcc	ttg	gcc	tcc	ttc	ctc	548
Leu	Cys	Ala	Ile	Phe	Cys	Cys	Phe	Leu	Val	Ala	Leu	Ala	Ser	Phe	Leu	
	135					140					145					
agg	cgt	aga	gga	gag	cca	cta	ccc	agc	cag	cct	gcc	ggg	cca	cgt	ggg	596
Arg	Arg	Arg	Gly	Glu	Pro	Leu	Pro	Ser	Gln	Pro	Ala	Gly	Pro	Arg	Gly	
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Ser	Gln	Ala	Asn	Ser	Pro	His	Ala	His	Arg	Pro	Val	Thr	Glu	Ala	Cys	
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gac	gag	gtg	acc	gcg	tca	ccc	cag	cct	gtg	gaa	acg	tgt	agc	ttc	tgc	692
Asp	Glu	Val	Thr	Ala	Ser	Pro	Gln	Pro	Val	Glu	Thr	Cys	Ser	Phe	Cys	
			185				190						195			
ttc	ccg	gag	cgc	agt	tct	ccc	act	cag	gag	agc	gcg	ccg	cgt	tcg	ctc	740
Phe	Pro	Glu	Arg	Ser	Ser	Pro	Thr	Gln	Glu	Ser	Ala	Pro	Arg	Ser	Leu	
	200					205						210				
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Gly	Ile	His	Gly	Phe	Ala	Gly	Thr	Ala	Ala	Pro	Gln	Pro	Cys	Met	Arg	
	215					220					225					
gca	aca	gta	ggc	ggc	ctg	ggt	gtc	ctg	cgc	gca	tcc	act	ggg	gac	gct	836
Ala	Thr	Val	Gly	Gly	Leu	Gly	Val	Leu	Arg	Ala	Ser	Thr	Gly	Asp	Ala	
230					235					240					245	
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Arg	Pro	Ala	Thr													
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tc																1430

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<223> Northern Blot Probe

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gaagttgaaa	acaattcaga	caactcggga	aggtaccaag	gattggagca	cagaggctca	360
gaagcaagtc	cagctctccc	ggggctgaag	ctgagtgcag	atcaggtggc	cctggtctac	420
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<223> ZC20061

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<211> 256

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 atcagggtctc ctgggcatgg ctaacattga cctggaaaag agcaggactg gtgatgaaat 180
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<400> 30
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<400> 31
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ccttaagaaa	agagaagaaa	tgaaactgaa	ggagtgtgtt	tccatcctcc	cacggaagga	240
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<210> 39
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<220>

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cgaggaagag	cggggcgagc	gacgggcaga	ggagaagggg	cggctgggag	acctgtgggt	720

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<220>
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<400> 52
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<210> 53

<212> DNA

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<400> 57

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<210> 58

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<220>

<223> Oligonucleotide primer

<400> 58

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<210> 59

<211> 20

<212> PRT

<213> Artificial Sequence

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<213> Artificial Sequence

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<223> Antibody peptide

<400> 60

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Val Lys Glu Thr
20

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